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UniProtKB/Swiss-Prot entry P43336



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Entry information

Entry name	PHHC_PSEAE
Primary accession number	P43336
Secondary accession numbers	None
Integrated into Swiss-Prot on	November 1, 1995
Sequence was last modified on	December 8, 2000 (Sequence version 2)
Annotations were last modified on	March 7, 2006 (Entry version 40)
Name and origin of the protein	
Protein name	Aromatic-amino-acid aminotransferase
Synonym	EC 2.6.1.57
Gene name	Name: phhC
	OrderedLocusNames: PA0870
From	Pseudomonas aeruginosa [TaxID: 287] [HAMAP proteor
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas

References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=ATCC 15692 / PAO1;
PubMed=8108417 [NCBI, ExPASy, EBI, Israel, Japan]
Zhao G., Xia T., Song J., Roy R.A.;
"Pseudomonas aeruginosa possesses homologues of mammalian phenylalanine hydroxyl and 4 alpha-carbinolamine dehydratase/DCoH as part of a three-component gene cluster. Proc. Natl. Acad. Sci. U.S.A. 91:1366-1370(1994).
- [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 15692 / PAO1;
DOI=10.1038/35023079; PubMed=10984043 [NCBI, ExPASy, EBI, Israel, Japan]
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkm. F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E.,

Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A.,  , Olsor M.V.;

"Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen. Nature 406:959-964(2000).

Comments

- **CATALYTIC ACTIVITY:** An aromatic amino acid + 2-oxoglutarate = an aromatic oxo acid + L-glutamate.
- **COFACTOR:** Pyridoxal phosphate.
- **SUBUNIT:** Homodimer (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasm.
- **SIMILARITY:** Belongs to the class-I pyridoxal-phosphate-dependent aminotransferase family.

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Cross-references

Sequence databases

EMBL	M88627; AAA25938.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	AE004522; AAG04259.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	D83535; D83535.	

3D structure databases

HSSP	P00509; 1ART. [HSSP ENTRY / SWISS-3DIMAGE / PDB]
ModBase	P43336.

Protein-protein interaction databases

DIP	P43336.
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Enzyme and pathway databases

BioCyc	PAER287:PA0870-MONOMER; -.
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2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HOGONOM	[Family / Alignment / Tree]
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Family and domain databases

InterPro	IPR004839; Aminotrans_I/II.
	IPR000796; Asp_trans.
	IPR004838; NHtransf_1_BS.
	Graphical view of domain structure.
PANTHER	PTHR11879; Asp_trans; 1.
Pfam	PF00155; Aminotran_1_2; 1.
	Pfam graphical view of domain structure.
PRINTS	PR00799; TRANSAMINASE.
PROSITE	PS00105; AA_TRANSFER_CLASS_1; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]

BLOCKS P43336.

Genome annotation databases

GenomeReviews AE004091_GR; PA0870.

CMR P43336; PA0870.

Other

ProtoNet P43336.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords**Amino-acid biosynthesis; Aminotransferase; Aromatic amino acid biosynthesis; Complete proteome; Pyridoxal phosphate; Transferase.****Features**

Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	399	399	Aromatic-amino-acid aminotransferase.	PRO_00001
BINDING	247	247		Pyridoxal phosphate (covalent) (By similarity).	
CONFLICT	382	382		D -> H (in Ref. 1).	
CONFLICT	387	387		D -> G (in Ref. 1).	

Sequence information

Length: **399 AA** [This is the length of the unprocessed precursor] Molecular weight: **43273 Da** [This is the MW of the unprocessed precursor] CRC64: **B6162FE13EBDB6E1** is a checksum on the sequence

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      10      20      30      40      50      60
MSHFAKVARV PGDPILGLLD AYRNDPRADK LDLGVGVYKD AQGLTPILRS VKLAEQRLVE

      70      80      90     100     110     120
QETTKSYVGG HGDALFAARL AELALGAASP LLLEQRADAT QTPGGTGALR LAGDFIAHCL

     130     140     150     160     170     180
PGRGIWLSDP TWPIHETLFA AAGLKVSHYP YVSADNRLDV EAMLAGLERI PQGDVVLHHA

     190     200     210     220     230     240
CCHNPTGFDL SHDDWRRVLD VVRRRELLPL IDFAYQGFGD GLEEDAWAVR LFAGELPEVL

     250     260     270     280     290     300
VTSSCSKNFG LYRDRVGALI VCAQNAEKL TDLRSQLAFLA RNLWSTPPAH GAEVVAAILG

     310     320     330     340     350     360
DSELKGLWQE EVEGMRSRIA SLRIGLVEAL APHGLAERFA HVGAQRGMFS YTGLSPQQVA

     370     380     390
RLRDEHAVYL VSSGRANVAG LDARRLDRLA QAIAQVCAD

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Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to
SWISS-MODEL



NPSA Sequence
analysis tools



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[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name	TYRB_ECOLI
Primary accession number	P04693
Secondary accession numbers	None
Integrated into Swiss-Prot on	August 13, 1987
Sequence was last modified on	August 13, 1987 (Sequence version 1)
Annotations were last modified on	March 7, 2006 (Entry version 62)

Name and origin of the protein

Protein name	Aromatic-amino-acid aminotransferase
Synonyms	EC 2.6.1.57 AROAT ARAT

Gene name	Name: tyrB
From	OrderedLocusNames: b4054
Taxonomy	Escherichia coli [TaxID: 562] [HAMAP proteome] Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
PubMed=3521591 [NCBI, ExPASy, EBI, Israel, Japan]
Fotheringham I.G., Dacey S.A., Taylor P.P., Smith T.J., Hunter M.G., Finlay M.E., Primros S.B., Parker D.M., Edwards R.M.;
"The cloning and sequence analysis of the aspC and tyrB genes from Escherichia coli K1: Comparison of the primary structures of the aspartate aminotransferase and aromatic aminotransferase of E. coli with those of the pig aspartate aminotransferase isoenzymes." Biochem. J. 234:593-604(1986).
- [2] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=K12;

PubMed=3907634 [NCBI, ExPASy, EBI, Israel, Japan]
 Kuramitsu S., Inoue K., Ogawa T., Ogawa H., Kagamiyama H.;
 "Aromatic amino acid aminotransferase of Escherichia coli: nucleotide sequence of the tyr gene.";

Biochem. Biophys. Res. Commun. 133:134-139(1985).

[3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=K12 / MG1655;

PubMed=8265357 [NCBI, ExPASy, EBI, Israel, Japan]

Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.;

"Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92 minutes.";

Nucleic Acids Res. 21:5408-5417(1993).

[4] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-39.

STRAIN=K12;

PubMed=3308851 [NCBI, ExPASy, EBI, Israel, Japan]

Yang J., Pittard J.;

"Molecular analysis of the regulatory region of the Escherichia coli K-12 tyrB gene.";

J. Bacteriol. 169:4710-4715(1987).

[5] X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).

DOI=10.1107/S0907444999006630; PubMed=10417420 [NCBI, ExPASy, EBI, Israel, Jap

Ko T.-P., Wu S.-P., Yang W.-Z., Tsai H., Yuan H.S.;

"Crystallization and preliminary crystallographic analysis of the Escherichia coli tyrosine aminotransferase.";

Acta Crystallogr. D 55:1474-1477(1999).

Comments

- **CATALYTIC ACTIVITY:** An aromatic amino acid + 2-oxoglutarate = an aromatic oxo ac L-glutamate.
- **COFACTOR:** Pyridoxal phosphate.
- **PATHWAY:** Biosynthesis of Phe, Tyr, Asp and Leu.
- **SUBUNIT:** Homodimer.
- **SUBCELLULAR LOCATION:** Cytoplasm.
- **SIMILARITY:** Belongs to the class-I pyridoxal-phosphate-dependent aminotransferase family.

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Cross-references

Sequence databases

	X03628; CAA27278.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	M12047; AAA24703.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
EMBL	U00006; AAC43148.1; -;	[EMBL / GenBank / DDBJ]
	Unassigned_DNA.	[CoDingSequence]
	U00096; AAC77024.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	M17809; AAA24704.1; -;	[EMBL / GenBank / DDBJ]

Genomic_DNA.	[CoDingSequence]
A01447; CAA00164.1; -;	[EMBL / GenBank / DDBJ]
Unassigned_DNA.	[CoDingSequence]

PIR A30379; XNECY.

3D structure databases

PDB 3TAT; X-ray; A/B/C/D/E/F=1-397.[ExPASy / RCSB / EBI]

ModBase P04693.

Protein-protein interaction databases

DIP P04693.

Enzyme and pathway databases

BioCyc EcoCyc:TYRB-MONOMER; -.

2D gel databases

ECO2DBASE E036.0; 6TH EDITION.

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Organism-specific gene databases

EchoBASE EB1033; -.

EcoGene EG11040; tyrB.

HOGENOM [Family / Alignment / Tree]

Family and domain databases

InterPro IPR004839; Aminotrans_I/II.
IPR000796; Asp_trans.
IPR004838; NHtransf_1_BS.
Graphical view of domain structure.

PANTHER PTHR11879; Asp_trans; 1.

Pfam PF00155; Aminotran_1_2; 1.
Pfam graphical view of domain structure.

PRINTS PR00799; TRANSAMINASE.

PROSITE PS00105; AA_TRANSFER_CLASS_1; 1.

ProDom [Domain structure / List of seq. sharing at least 1 domain]

BLOCKS P04693.

Genome annotation databases

GenomeReviews U00096_GR; b4054.

CMR P04693; b4054.

Other

ProtoNet P04693.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

**3D-structure; Amino-acid biosynthesis; Aminotransferase;
Aromatic amino acid biosynthesis; Complete proteome; Pyridoxal phosphate; Transfe**

Features



Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	397	397	Aromatic-amino-acid aminotransferase.	PRO_0000123892
BINDING	66	66		Substrate (<i>By similarity</i>).	
BINDING	247	247		Pyridoxal phosphate (covalent).	
BINDING	281	281		Substrate (<i>By similarity</i>).	
TURN	12	15	4		
HELIX	16	22	7		
STRAND	23	23	1		
STRAND	26	27	2		
STRAND	29	30	2		
STRAND	32	32	1		
STRAND	35	35	1		
TURN	39	40	2		
STRAND	41	42	2		
HELIX	47	56	10		
TURN	57	58	2		
STRAND	59	59	1		
STRAND	62	64	3		
TURN	69	70	2		
HELIX	73	83	11		
TURN	84	84	1		
STRAND	86	87	2		
HELIX	89	92	4		
TURN	93	94	2		
STRAND	96	98	3		
STRAND	101	102	2		
HELIX	103	118	16		
STRAND	120	121	2		
STRAND	125	126	2		
STRAND	128	129	2		
TURN	132	133	2		
HELIX	134	139	6		
TURN	140	142	3		
STRAND	146	147	2		
TURN	153	155	3		
STRAND	156	157	2		
HELIX	160	167	8		
TURN	168	169	2		
STRAND	172	173	2		
STRAND	177	178	2		
STRAND	180	182	3		
STRAND	184	186	3		
HELIX	192	204	13		
TURN	205	206	2		
STRAND	210	211	2		
STRAND	213	214	2		

TURN	216	217	2
STRAND	218	220	3
HELIX	222	233	12
TURN	234	236	3
STRAND	240	241	2
STRAND	243	243	1
HELIX	246	249	4
TURN	250	250	1
STRAND	251	251	1
TURN	252	254	3
STRAND	257	257	1
STRAND	260	262	3
STRAND	264	265	2
TURN	266	267	2
HELIX	268	279	12
TURN	280	284	5
STRAND	285	286	2
STRAND	289	289	1
HELIX	290	298	9
TURN	299	300	2
STRAND	301	301	1
HELIX	302	328	27
TURN	329	333	5
TURN	335	336	2
STRAND	337	337	1
TURN	339	340	2
HELIX	341	344	4
STRAND	347	349	3
HELIX	356	362	7
TURN	363	366	4
STRAND	368	369	2
STRAND	372	374	3
STRAND	377	377	1
TURN	378	379	2
STRAND	380	380	1
TURN	383	385	3
HELIX	386	396	11

Sequence information

Length: **397 AA** [This is the length of the unprocessed precursor]

Molecular weight: **43538 Da** [This is the MW of the unprocessed precursor]

CRC64: **46E69B4B8378BA6B** is a checksum on the sequence

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MFQKVDAYAG	DPILTLMERF	KEDPRSDKVN	LSIGLYYNED	GIIPQLQAVA	EAEARLNAQP
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
HGASLYLPME	GLNCYRHAIA	PLLFGADHPV	LKQQRVATIQ	TLGGSGALKV	GADFLKRYFP

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      130      140      150      160      170      180
ESGVVWSDPT WENHVAIFAG AGFEVSTYPW YDEATNGVRF NDLLATLCTL PARSIVLLHP

      190      200      210      220      230      240
CCHNPTGADL TNDQWDAVIE ILKARELIPF LDIAYQGFGA GMEEDAYAIR AIASAGLPAL

      250      260      270      280      290      300
VSNSFSKIFS LYGERVGGLS VMCEDAEAAG RVLGQLKATV RRNYSSPPNF GAQVVAAVLN

      310      320      330      340      350      360
DEALKASWLA EVEEMRTRIL AMRQELVKVL STEMPERNFD YLLNQGMFS YTGLSAAQVD

      370      380      390
RLREEFGVYL IASGRMCVAG LNTANVQRVA KAFAAVM

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PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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analysis tools



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